

SEQUENCE LISTING

<110> Ruben et al.

<120> Cytokine Receptor Common Gamma Chain Like

<130> PF466P2

<150> 60/269,876

<151> 2001-02-21

<150> PCT/US00/22493

<151> 2000-08-17

<150> 09/376,430

<151> 1999-08-18

<150> 09/263,626

<151> 1999-03-05

<150> PCT/US99/05068

<151> 1999-03-05

<150> 60/086,505

<151> 1998-05-22

<150> 60/078,563

<151> 1998-03-19

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 1573

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(1125)

<400> 1

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Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe  
1 5 10

ctg ctg gga ggc tgg atg gct ttg ggg caa gga gca gca gaa gga 99  
Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Ala Ala Glu Gly  
15 20 25

gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca 147  
Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr  
30 35 40 45

tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga 195  
Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg  
50 55 60

ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln	65	70	75	243
gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp	80	85	90	291
att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala	95	100	105	339
agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val	110	115	120	387
aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu	130	135	140	435
tcc tac ggg gat ctc ctc tat gag gtt cag tac ccg agc ccc ttc gac Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp	145	150	155	483
acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu	160	165	170	531
ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala	175	180	185	579
atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu	190	195	200	627
gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr	210	215	220	675
cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser	225	230	235	723
ctg gcc atc ctt ctg atg gtg tct ctc ctt ctg tct tta tgg aaa Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys	240	245	250	771
tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys	255	260	265	819
tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu	270	275	280	867
tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly	290	295	300	915

gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc	963
Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala	
305	310
315	
aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag	1011
Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu	
320	325
330	
aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa	1059
Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln	
335	340
345	
ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac	1107
Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp	
350	355
360	365
cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt	1155
Arg Ser Tyr Val Ala Leu	
370	
caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccaccat	1215
ggatggaaag tctccacgcc aatgatggta ggactaggag actctgaaga cccagcctca	1275
ccgcctaattg cggccactgc cctgctaact ttccccaca tgagtctctg tgttcaaagg	1335
cttgatggca gatgggagcc aattgctcca ggagattac tcccagttcc tttcgtgcc	1395
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<210> 2  
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 <212> PRT  
 <213> Homo sapiens

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Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile			
20	25	30	
Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala			
35	40	45	
Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly			
50	55	60	
Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His			
65	70	75	80
Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr			
85	90	95	

Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
 100 105 110  
 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser  
 115 120 125  
 Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly  
 130 135 140  
 Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp  
 145 150 155 160  
 Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp  
 165 170 175  
 Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp  
 180 185 190  
 Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys  
 195 200 205  
 Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro  
 210 215 220  
 Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile  
 225 230 235 240  
 Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg  
 245 250 255  
 Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe  
 260 265 270  
 Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr  
 275 280 285  
 Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln  
 290 295 300  
 Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu  
 305 310 315 320  
 Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala  
 325 330 335  
 Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp  
 340 345 350  
 Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp Arg Ser Tyr  
 355 360 365  
 Val Ala Leu  
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<210> 3  
 <211> 379

<212> PRT

<213> Homo sapiens

<400> 3

Met Leu Lys Pro Pro Leu Pro Leu Arg Ser Leu Leu Phe Leu Gln Leu  
1 5 10 15

Pro Leu Leu Gly Val Gly Leu Asn Pro Lys Phe Leu Thr Pro Ser Gly  
20 25 30

Asn Glu Asp Ile Gly Gly Lys Pro Gly Thr Gly Asp Phe Phe Leu  
35 40 45

Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro  
50 55 60

Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp  
65 70 75 80

Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly  
85 90 95

Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr  
100 105 110

Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu  
115 120 125

Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu  
130 135 140

His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile  
145 150 155 160

Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln  
165 170 175

Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His  
180 185 190

Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser  
195 200 205

Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys  
210 215 220

Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser  
225 230 235 240

Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn  
245 250 255

Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala  
260 265 270

Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser  
275 280 285

Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro

290

295

300

Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe  
305 310 315 320

Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro  
325 330 335

Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly  
340 345 350

Gly Glu Gly Pro Gly Gly Ser Pro Cys Ser Gln His Ser Pro Tyr Trp  
355 360 365

Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Pro  
370 375

<210> 4  
<211> 733  
<212> DNA  
<213> Homo sapiens

<400> 4  
ggatccgga gcccaaatct tctgacaaaaa ctcacacatg cccaccgtgc ccagcacctg 60  
aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120  
tctcccgac tcctgaggc acatgcgtgg tggtgacgt aagccacgaa gaccctgagg 180  
tcaagttcaa ctggtaacgtg gacggcgtgg aggtgcataa tgccaaagaca aagccgcggg 240  
aggagcgtta caacagcacg taccgtgtgg tcagcgtcct caccgtccctg caccaggact 300  
ggctgaatgg caaggagttac aagtgcacagg tctccaacaa agccctccca acccccatcg 360  
agaaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggc aaaggcttct 480  
atccaagcga catcggcgtg gagtgggaga gcaatggca gccggagaaac aactacaaga 540  
ccacgcctcc cgtgctggac tccgacggct ccttccttct ctacagcaag ctcaccgtgg 600  
acaagagcag gtggcagcag gggAACgtct tctcatgctc cgtatgcat gaggctctgc 660  
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720  
gactcttagag gat 733

<210> 5  
<211> 5  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (3)  
<223> Xaa equals any amino acid

<400> 5  
Trp Ser Xaa Trp Ser  
1 5

<210> 6  
<211> 86  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Primer\_Bind  
<223> Synthetic sequence with 4 tandem copies of the GAS binding site found in the IRF1 promoter (Rothman et al., Immunity 1:457-468 (1994)), 18 nucleotides complementary to the SV40 early promoter, and a Xho I restriction site.

<400> 6  
gcgcctcgag atttccccga aatcttagatt tcccccgaat gattcccccg aaatgatttc 60  
cccgaaatat ctgccatctc aattag 86

<210> 7  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Primer\_Bind  
<223> Synthetic sequence complementary to the SV40 promoter; includes a Hind III restriction site.

<400> 7  
gcggcaagct ttttgcaaag cctaggc 27

<210> 8  
<211> 271  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Protein\_Bind  
<223> Synthetic promoter for use in biological assays; includes GAS binding sites found in the IRF1 promoter (Rothman et al., Immunity 1:457-468 (1994)).

<400> 8  
ctcgagatt cccccgaaatc tagatttccc cgaaatgatt tcccccgaat gattcccccg 60  
aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120  
gcccctaact ccgccccagg ttccgccccat ggctgactaa ttttttttat 180  
ttatgcagag gcccggccg ctcggccctc tgagctattc cagaagtatg gaggaggctt 240  
ttttggaggc ctaggctttt gaaaaagct t 271

<210> 9  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Primer\_Bind  
<223> Synthetic primer complementary to human genomic EGR-1 promoter sequence (Sakamoto et al., Oncogene 6:867-871 (1991)); including an Xho I restriction site.

<400> 9  
gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 10  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> Primer\_Bind  
 <223> Synthetic primer complementary to human genomic EGR-1 promoter sequence (Sakamoto et al., Oncogene 6:867-871 (1991)); including an Hind III restriction site.  
  
 <400> 10  
 gcgaagcttc gcgactcccc ggatccgcct c

31

<210> 11  
 <211> 12  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 11  
 ggggactttc cc

12

<210> 12  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> Primer\_Bind  
 <223> Synthetic primer with 4 tandem copies of the NF-KB binding site (GGGGACTTTCCC), 18 nucleotides complementary to the 5' end of the SV40 early promoter sequence, and a XhoI restriction site.  
  
 <400> 12  
 gcggcctcg a ggggactttc ccggggactt tccggggact ttccggact ttccatcctg 60  
 ccatctcaat tag

73

<210> 13  
 <211> 256  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <221> Protein\_Bind  
 <223> Synthetic promoter for use in biological assays; including NF-KB binding sites.  
  
 <400> 13  
 ctcgaggggga ctttccccgg gactttccgg ggactttccg ggactttcca tctgccatct 60  
 caatttagtca gcaaccatag tcccgccccct aactccgccc atcccgcccc taactccgccc 120  
 cagttccgccc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180  
 ggccgcctcg gcctctgagc tattccagaa gtatgtgagga gcctttttg gaggcctagg 240  
 ctttgcaaa aagctt

256

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<221> Primer\_Bind  
<223> Synthetic primer containing the Nco I restriction site followed a number of nucleotides of the amino terminal coding sequence of CRCGCL

<400> 14  
gttaggcat gggaggagca gcagaaggca 29

<210> 15  
<211> 33  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<221> Primer\_Bind  
<223> Synthetic primer containing the BglII restriction site followed by a number nucleotides complementary to the 3' end of the coding sequence of CRCGCL

<400> 15  
ggttaaagat ctcaacgcca cgttaggagcg gtc 33

<210> 16  
<211> 38  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<221> Primer\_Bind  
<223> Synthetic primer to amplify the cDNA sequence encoding the full length CRCGCL protein including the AUG initiation codon and the naturally associated leader,also contains a BglII site, and Kozak signal

<400> 16  
ccggtagat ctgccatcat ggctttgggg caaggagg 38

<210> 17  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<221> Primer\_Bind  
<223> Synthetic primer containing the XbaI restriction site followed by a number of nucleotides complementary to the 3' noncoding sequence of SEQ ID NO:1  
  
<400> 17  
ccggtttctta gatcacaagg ccacgttagga gcggtc 36

<210> 18  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (1)  
<223> Xaa equals Ser, Thr, Gly or Leu

<220>  
<221> SITE  
<222> (2)  
<223> Xaa equals any amino acid

<220>  
<221> SITE  
<222> (4)  
<223> Xaa equals Ser or Gly

<220>  
<221> SITE  
<222> (5)  
<223> Xaa equals any amino acid

<400> 18  
Xaa Xaa Trp Xaa Xaa Trp Ser  
1 5

<210> 19  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (2)  
<223> Xaa equals any amino acid

<220>  
<221> SITE  
<222> (5)  
<223> Xaa equals any amino acid

<400> 19  
Thr Xaa Pro Ser Xaa Trp Ser  
1 5

<210> 20  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE

<222> (2)  
<223> Xaa equals Pro or Glu

<220>  
<221> SITE  
<222> (3)  
<223> Xaa equals any amino acid

<220>  
<221> SITE  
<222> (4)  
<223> Xaa equals Val or Ile

<220>  
<221> SITE  
<222> (6)  
<223> Xaa equals Asn, Ser or Asp

<400> 20  
Trp Xaa Xaa Xaa Pro Xaa Pro  
1 5

<210> 21  
<211> 7  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (3)  
<223> Xaa equals any amino acid

<400> 21  
Ile Pro Xaa Val Pro Asp Pro  
1 5

<210> 22  
<211> 54  
<212> PRT  
<213> Homo sapiens

<400> 22  
Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp  
1 5 10 15

Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe  
20 25 30

Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu  
35 40 45

Gly His Thr Ser Gly Cys  
50

<210> 23  
<211> 30

<212> PRT

<213> Homo sapiens

<400> 23

Arg Arg His Ser Leu Phe Leu His Gln Glu Trp Asp Ala Pro Arg Phe  
1 5 10 15

His Arg Lys Ser Leu Asp Gly Leu Leu Pro Glu Thr Gln Phe  
20 25 30

<210> 24

<211> 81

<212> PRT

<213> Homo sapiens

<400> 24

Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp Gln  
1 5 10 15

Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp Ala  
20 25 30

Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp Val  
35 40 45

Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys Trp  
50 55 60

Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro Pro  
65 70 75 80

Lys

<210> 25

<211> 181

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (68)

<223> Xaa equals any amino acid

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<221> SITE

<222> (73)

<223> Xaa equals any amino acid

<220>

<221> SITE

<222> (88)

<223> Xaa equals any amino acid

<400> 25

Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu  
1 5 10 15

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20								25						30	
Pro	Thr	Pro	Pro	Lys	Pro	Lys	Leu	Ser	Lys	Phe	Ile	Leu	Ile	Ser	Ser
35							40						45		
Leu	Ala	Ile	Leu	Leu	Met	Val	Ser	Leu	Leu	Leu	Ser	Leu	Trp	Lys	
50						55					60				
Leu	Trp	Arg	Xaa	Lys	Lys	Phe	Leu	Xaa	Pro	Ser	Val	Pro	Asp	Pro	Lys
65						70				75					80
Ser	Ile	Phe	Pro	Gly	Leu	Phe	Xaa	Ile	His	Gln	Gly	Asn	Phe	Gln	Glu
									85	90				95	
Trp	Ile	Thr	Asp	Thr	Gln	Asn	Val	Ala	His	Leu	His	Lys	Met	Ala	Gly
							100			105			110		
Ala	Glu	Gln	Glu	Ser	Gly	Pro	Glu	Glu	Pro	Leu	Val	Val	Gln	Leu	Ala
							115			120			125		
Lys	Thr	Glu	Ala	Glu	Ser	Pro	Arg	Met	Leu	Asp	Pro	Gln	Thr	Glu	Glu
							130			135			140		
Lys	Glu	Ala	Ser	Gly	Gly	Ser	Leu	Gln	Leu	Pro	His	Gln	Pro	Leu	Gln
							145			150			155		160
Gly	Gly	Asp	Val	Val	Thr	Ile	Gly	Gly	Phe	Thr	Phe	Val	Met	Asn	Asp
							165			170			175		
Arg	Ser	Tyr	Val	Ala											
							180								

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<210> 26
<211> 1567
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (830)
<223> n equals a, t, g or c

<220>
<221> misc_feature
<222> (416)
<223> y equals c or t

<220>
<221> misc_feature
<222> (784)
<223> m equals a or c

<220>
<221> misc_feature
<222> (785)
<223> y equals c or t

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<400> 26  
gggcatgggg cggtcggttc tgctgtgggg agctgccgtc ttctcgctgg gaggctggat 60  
ggcttgggg caaggaggag cagcagaagg agtacagatt caratcatct acttcaattt 120  
agaaaccgtg caggtgacat ggaatgccag caaatactcc aggacaacc tgactttcca 180  
ctacagattc aacggtgatg aggctatga ccagtgcacc aactacccctc tccaggaagg 240  
tcacacttcg ggggcctcc tagacgcasa gcagcgagac gacattctct atttctccat 300  
caggaatggg acgcaccccg ttttcaccgc aagtcgctgg atggtttattt acctgaaacc 360  
cagttccccg aagcacgtga gatttcgtgg catcaggaaw gacggtgacg tgttcycgac 420  
ctgtcctacg gggatctctt ctagggatc cagtaccggc gcccccttcga caccgagttgg 480  
cagtccaaac aggaaaatac ctgcaacgtc accatagaag gttggatgc cgagaagtgt 540  
tacttttctt gggtcagggt gaaggctatg gaggatgtat atggggcaga cacataccca 600  
agcgacttgt cagaggtgac atgctggcag agaggcgaga ttccggatgc ctgtgcagag 660  
acaccaacgc ctcccaaacc aaagctgtcc aaattttattt taatttccag cctggccatc 720  
cttctgtatgg tggctctctt cttctgtct ttatggaaat tatggagart gaagaagtt 780  
ctcmytccca gctgtccaga cccgaaatcc atttcccccg ggctcttgn tatacaccaa 840  
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ggcgcagagc aagaaagtgg ccccgaggag cccctggtag tccagggtggc caagactgaa 960  
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<210> 27  
<211> 170  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (89)  
<223> Xaa equals any amino acid

<220>  
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<223> Xaa equals any amino acid

<220>  
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Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile  
20 25 30

Gln Ile Ile Tyr Phe Asp Leu Glu Thr Val Gln Val Thr Tyr Asp Ala

35 40 45  
Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
50 55 60

Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
65 70 75 80

Thr Ser Gly Cys Leu Leu Asp Ala Xaa Gln Arg Asp Asp Ile Leu Tyr  
85 90 95

Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
100 105 110

Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Arg  
115 120 125

Gly Ile Arg Xaa Asp Gly Asp Val Phe Xaa Thr Cys Pro Thr Gly Ile  
130 135 140

Ser Ser Met Arg Phe Ser Thr Gly Ala Pro Ser Thr Pro Ser Gly Ser  
145 150 155 160

Pro Asn Arg Lys Ile Pro Ala Thr Ser Pro  
165 170

<210> 28  
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<212> DNA  
<213> Artificial Sequence

<220>  
<221> Primer\_Bind  
<223> Synthetic primer to amplify the cDNA sequence encoding the amino acids Met 1 to Lys 231 including the AUG initiation codon and the naturally associated leader, also contains a BglII site, and Kozak signal

<400> 28  
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<210> 29  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> Primer\_Bind  
<223> Synthetic primer to amplify the cDNA sequence encoding the amino acids Met 1 to Lys 231, also contains a BglII site

<400> 29  
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<213> Homo sapiens

<220>

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<222> (2)

<223> Xaa equals any amino acid

<400> 30

Trp Xaa Trp Ser

1

<210> 31

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer\_Bind

<223> Synthetic primer to amplify the cDNA sequence encoding the amino acids Met 1 to Lys 231, also contains a XbaI site

<400> 31

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<210> 32

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer\_Bind

<223> Synthetic primer to amplify DNA encoding amino acids M1-K231 of SEQ ID NO:2, contains a BglII restriction site.

<400> 32

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gccatcatgg ggcggctggc tctg 144